

SEQUENCE LISTING

<110> NELSON, DAVID R.

5 <120> A LIVE, AVIRULENT STRAIN OF V. ANGUILLARUM THAT
PROTECTS FISH AGAINST INFECTION BY VIRULENT V.
ANGUILLARUM

<130> 5112

<140>

<141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 3609

<212> DNA

<213> V. Anguillarum

<220>

<223> "n" bases may be a, t, c, g, other or unknown

<400> 1

```

gtcgacttat tgcattgatg gcgtacatgg tagtgccatc cttcgtttgc taacaagcgt 60
tgtataaaaag cttggtcggt ttcacacaagt tgaacacaat actcatgatt tttcccactt 120
ccggaaaaggg aaaagtgaaa atagcttttg agatcagcct gttctagcag cttttcaatg 180
atctttttcg tcggttacgtt ttgaaaaatc tgacgactgc gtttgatttg caacaagcta 240
agtggatcca atatctctat ttgataataa aactgctgct tgtctttgct atactctgtg 300
aattgcagag tgctacatat acctgaaaaa aaacgctttc cagaatctaa ttcgtaagac 360
acacaaacag ctttacctag gtttttggtg tcgatctcca tgtttgcccgc gatggaaaacg 420
gaaaactgac acccgccgga tacgcttttc tctccgatta attgcgtgac aatataactt 480
ttgctatctg aaagcttaat ggtgagggag cgggtttggt gctttaattc gttactgctc 540
atattcaatt aattcactat taaataaaca gttctaaaag gctgtttatt ggatgaatat 600
tcgaaattat cacataataa ttgatgctat tattacttgc tgtattggta tcaactttca 660
tgctctatac atgtaatat tttcgagtta gaccttaatt caaggtaatt tgtctattta 720
attattatct gaataatatg taatcgattg ctttgtggtt atttttatgt ttgtttcatt 780
tttaatgacg gtgagottgt gcattcatat tttttatgat gacaacatct ttgatgaagt 840
atttaagata ttgttaatgc atgaggggtt tgcgtgtatt ttttatatta aatcataata 900
aatcaacaa tatatgttat tttgtgtctt tttatagtgt tcttttaaag aggtaggatg 960
acctaaaggt cgcctagaaa tatggcgtaa attgccattg ctataattca cctcaaagat 1020
acactatttg caaattgaca aatatgtcac ttcgatgaa acaatattag tagatgttgt 1080
ttttgctgca aaaataaaaa tttttctggt tgaataaact caaggcctct agcgttttcc 1140
tttatcttaa aatacaggaa atagcgattg aagttaattg aacttaagc aasdramgaa 1200
tagtcaacct aacagagcag gaacctatgc ctttgtcaaa gcatcaaatt gagcaacttt 1260
ctaaacctct gagtgatgat tcgatctgtg gcgtttatct taaactggaa aaaagtgcctt 1320
ttcgcccatt acgtaatgaa tttaatgtcg cgcaaactgc gctgcgtaag ctaagtcaaa 1380
accctagtgc tgacgagaga gatgcgttac aagaggcatg tctaaataag tggaagattc 1440
tctctgacag tttgtacgaa cagttttcaa aaacaaccag agatatcgag ctcatctcat 1500
ggtttggtgc tgctcaattc cttctcgata ccacattaga aagtgcgtgc aatagccttg 1560
agtggttagc ggatttaagt gagaagcaact gggatcacct caaccctgta ctaccagttg 1620
aaacgctcaa atctgatgat gataagggca aagaaagaga gcaagcagat gcgaaagtta 1680
aagcattttt ccaactagtc ggcgatagcg aggaaagctc gattctctat gcgcccgtgc 1740
tgcaactgcc cttagtcggg gaagtgcgtt tttttgactt tcaaagtgca gagagaaaag 1800
gcgaaatcag ccaactgaaa tctatgctta cgaccacggt ggcgcaagag cgtttcgcaa 1860

```

5
 10
 15
 20
 25
 30

```

ttcaattcaa gatggaac gccaaacggt gtgtcaccca attagatcgt ttgtcagcgt 1920
tggtgagcac taagtgtcat tctctaggca gtcaaagtac caacttcgga ttgccaagt 1980
cactgcttac cgtgttgaa aacgctttgg ttcattctaa tggaattaag ttagcaccga 2040
aagcggaggc caagacagta gagcaagagg ttgccgaaag ttcagtttct gaaggggagc 2100
tgccaagcca tatggatata aaacatatag agcgaatacc gatggcatca gagcaggctc 2160
agaccgtaag ccaacactta cagcgaggaa acctctctga actgggtaat ttaaacaata 2220
tgaaccgaga ctttagctttc catttggtga gagaagtctc tgattatttt cgccagagcg 2280
aaccgcatag cccaatttca tttttgtag aaaaagcgat tcgatgggga tatttatcct 2340
tacctgagtt gctgcgagaa atgatgtcgg aacaaaacgg tgacgctctt agtacgattt 2400
ttaatgccgc cggattgaat catctcgatc aggttttgct gccggagggt agtactcca 2460
cggtgggcat tgaaagcccc caaacacctc aagcgaagcc ttccgtttcg gatccgcgaa 2520
gtgttgaaga gcatgtatct cagacttccc ctgtagatac ccaatctaag caagatcaaa 2580
aaccacaatc atccgcta*s drbcgtcggc tctgagttgg taattgtgtt taaaaataa 2640
ggaaaaatca tggcaagtat ttacatgcgt gtaagcggtc ttcaagttga gggcgagcg 2700
actatcggtc agctagaaac ggctgaagg aaaaatgacg gttggtttgc aatcaactct 2760
tactcttggg gtggcgctcg taacgttgct atggacatcg gtaacggcac caatgcggat 2820
tcaggcatgg ttggcgtaag cgaagttagc gtaactaaag aagtcgatgg tgcttctgaa 2880
gacctactgt cttattttatt caaccaggt aaagacggta aaactgttga ggttgcat 2940
actaagcctt ctaacgatgg tcaaggtgca gacgtttact tccaagttaa gctagaaaaa 3000
gcacgtttag tttcttataa cgtgagcggg actgacggat ctcaaccgta cgagagccta 3060
tctctttctt acacttctat ttctcagaag catcactatg agaaagaagg ttgtgaacta 3120
caaagcggtg gtgtgtgac ttacgacctc ccgaccggga aaa*tgactt ctggtgaagta 3180
attctttcat tagacatgcc acgttaattg gcatgtctat ttcatgaata tctcsdrcat 3240
tttaggacac cgttatggca ttgaactcac aacataagcg cgttagtaag aaccgtgtca 3300
gcatcaccta tgacgttgaa acgaatggcg ccgtaaagac gaaagagctg ccgtttgttg 3360
ttggcgctcat tggcgacttt tcaggacaca aaccagaatc agaaaaagtt gatttagaag 3420
agcgagagtt cacgggtatc gataaagaca acttcgatac agtgatgggg caaattcacc 3480
cgcgctcttc gtacaaggtt gataacaagc ttgctaatag tgatagccag tttgaagtga 3540
acttgagcct ccgttcgatg aaagatttcc acccagagaa cttagttgat naaattgagc 3600
cgcttaaag
  
```

<210> 2
 <211> 463
 <212> PRT
 <213> V. Anguillarum

40
 45
 50
 55

```

<400> 2
Met Pro Leu Ser Lys His Gln Ile Glu Gln Leu Ser Lys Pro Leu Ser
  1          5          10          15

Asp Asp Ser Ile Cys Gly Val Tyr Leu Lys Leu Glu Lys Ser Ala Phe
      20          25          30

Arg Pro Leu Arg Asn Glu Phe Asn Val Ala Gln Thr Ala Leu Arg Lys
      35          40          45

Leu Ser Gln Asn Pro Ser Ala Asp Glu Arg Asp Ala Leu Gln Glu Ala
      50          55          60

Cys Leu Asn Lys Trp Lys Ile Leu Ser Asp Ser Leu Tyr Glu Gln Phe
      65          70          75          80

Ser Lys Thr Thr Arg Asp Ile Glu Leu Ile Ser Trp Phe Val Ala Ala
      85          90          95

Gln Phe Leu Leu Asp Thr Thr Leu Glu Ser Ala Ala Asn Ser Leu Glu
  
```

	100	105	110
	Trp Leu Ala Asp Leu Ser Glu Lys His Trp Asp His Leu Asn Pro Val		
	115	120	125
5	Leu Pro Val Glu Thr Leu Lys Ser Asp Asp Asp Lys Gly Lys Glu Arg		
	130	135	140
10	Glu Gln Ala Asp Ala Lys Val Lys Ala Phe Phe Gln Leu Val Gly Asp		
	145	150	155
	Ser Glu Glu Ser Ser Ile Leu Tyr Ala Pro Val Leu Gln Leu Pro Leu		
	165	170	175
15	Val Gly Glu Val Thr Phe Phe Asp Phe Gln Ser Ala Glu Arg Lys Gly		
	180	185	190
	Glu Ile Ser Gln Leu Lys Ser Met Leu Thr Thr Thr Val Ala Gln Glu		
	195	200	205
20	Arg Phe Ala Ile Gln Phe Lys Met Glu Asn Ala Lys Arg Cys Val Thr		
	210	215	220
	Gln Leu Asp Arg Leu Ser Ala Leu Val Ser Thr Lys Cys His Ser Leu		
	225	230	235
25	Gly Ser Gln Ser Thr Asn Phe Gly Phe Ala Lys Ser Leu Leu Thr Arg		
	245	250	255
30	Val Glu Asn Ala Leu Val His Leu Ser Gly Ile Lys Leu Ala Pro Lys		
	260	265	270
	Ala Glu Ala Lys Thr Val Glu Gln Glu Val Ala Glu Ser Ser Val Ser		
	275	280	285
35	Glu Gly Glu Leu Pro Ser His Met Asp Thr Lys His Ile Glu Arg Ile		
	290	295	300
40	Pro Met Ala Ser Glu Gln Ala Gln Thr Val Ser Gln His Leu His Ala		
	305	310	315
	Gly Asn Leu Ser Glu Leu Gly Asn Leu Asn Asn Met Asn Arg Asp Leu		
	325	330	335
45	Ala Phe His Leu Leu Arg Glu Val Ser Asp Tyr Phe Arg Gln Ser Glu		
	340	345	350
	Pro His Ser Pro Ile Ser Phe Leu Leu Glu Lys Ala Ile Arg Trp Gly		
	355	360	365
50	Tyr Leu Ser Leu Pro Glu Leu Leu Arg Glu Met Met Ser Glu Gln Asn		
	370	375	380
55	Gly Asp Ala Leu Ser Thr Ile Phe Asn Ala Ala Gly Leu Asn His Leu		
	385	390	395
	Asp Gln Val Leu Leu Pro Glu Val Ser Thr Pro Thr Val Gly Ile Glu		

405 410 415
 Ser Pro Gln Thr Pro Gln Ala Lys Pro Ser Val Ser Asp Pro Arg Ser
 420 425 430
 5 Val Glu Glu His Val Ser Gln Thr Ser Pro Val Asp Thr Gln Ser Lys
 435 440 445
 10 Gln Asp Gln Lys Pro Gln Ser Ser Ala Thr Ser Ala Leu Ser Trp
 450 455 460

 15 <210> 3
 <211> 176
 <212> PRT
 <213> V. Anguillarum

 20 <400> 3
 Met Ala Ser Ile Tyr Met Arg Val Ser Gly Leu Gln Val Glu Gly Ala
 1 5 10 15
 Ala Thr Ile Gly Gln Leu Glu Thr Ala Glu Gly Lys Asn Asp Gly Trp
 20 25 30
 25 Phe Ala Ile Asn Ser Tyr Ser Trp Gly Gly Ala Arg Asn Val Ala Met
 35 40 45
 Asp Ile Gly Asn Gly Thr Asn Ala Asp Ser Gly Met Val Gly Val Ser
 50 55 60
 30 Glu Val Ser Val Thr Lys Glu Val Asp Gly Ala Ser Glu Asp Leu Leu
 65 70 75 80
 Ser Tyr Leu Phe Asn Pro Gly Lys Asp Gly Lys Thr Val Glu Val Ala
 85 90 95
 35 Phe Thr Lys Pro Ser Asn Asp Gly Gln Gly Ala Asp Val Tyr Phe Gln
 100 105 110
 40 Val Lys Leu Glu Lys Ala Arg Leu Val Ser Tyr Asn Val Ser Gly Thr
 115 120 125
 Asp Gly Ser Gln Pro Tyr Glu Ser Leu Ser Leu Ser Tyr Thr Ser Ile
 130 135 140
 45 Ser Gln Lys His His Tyr Glu Lys Glu Gly Gly Glu Leu Gln Ser Gly
 145 150 155 160
 Gly Val Val Thr Tyr Asp Leu Pro Thr Gly Lys Met Thr Ser Gly Lys
 165 170 175
 50

 55 <210> 4
 <211> 117
 <212> PRT
 <213> V. Anguillarum

 <220>

<223> "Xaa" may be any, other or unknown amino acid

<400> 4

5 Met Ala Leu Asn Ser Gln His Lys Arg Val Ser Lys Asn Arg Val Ser
1 5 10 15
Ile Thr Tyr Asp Val Glu Thr Asn Gly Ala Val Lys Thr Lys Glu Leu
20 25 30
10 Pro Phe Val Val Gly Val Ile Gly Asp Phe Ser Gly His Lys Pro Glu
35 40 45
Ser Glu Lys Val Asp Leu Glu Glu Arg Glu Phe Thr Gly Ile Asp Lys
50 55 60
15 Asp Asn Phe Asp Thr Val Met Gly Gln Ile His Pro Arg Leu Ser Tyr
65 70 75 80
Lys Val Asp Asn Lys Leu Ala Asn Asp Asp Ser Gln Phe Glu Val Asn
20 85 90 95
Leu Ser Leu Arg Ser Met Lys Asp Phe His Pro Glu Asn Leu Val Asp
100 105 110
25 Xaa Ile Glu Pro Leu
115